

GenMAPP Gene Database for *Saccharomyces pombe*

Sp-Std_20060502.gdb

ReadMe

This document contains the following:

1. Overview of the GenMAPP application and accessory programs
2. System Requirements and Compatibility
3. Installation Instructions
4. Gene Database Specifications
Gene ID Systems
5. Contact Information for support, bug reports, feature requests
6. Database Schema Diagram

1. Overview of the GenMAPP application and accessory programs

GenMAPP (Gene Map Annotator and Pathway Profiler) is a free computer application for viewing and analyzing DNA microarray and omics data while considering the biological context of genes and gene products. MAPPFinder is an accessory program that works with GenMAPP and Gene Ontology to identify global biological trends in the data. GenMAPP is a stand-alone application that requires a Gene Database for each species, MAPPs, and Expression Dataset files. The GenMAPP Gene Database (file with the extension .gdb) is used to relate gene IDs on MAPPs (.mapp, representations of pathways and other functional groupings of genes) to data in Expression Datasets (.gex, DNA microarray or other high-throughput data). This ReadMe describes a Gene Database for *Saccharomyces pombe* that was built by the National Institute of Pharmaceutical Education and Research (NIPER) Pharmacoinformatics Group in collaboration with Conklin group at the J. David Gladstone Institutes.

2. System Requirements and Compatibility

- This Gene Database is compatible with GenMAPP 2.0 and 2.1 and MAPPFinder 2.0. These programs can be downloaded from <http://www.genmapp.org>
- The database and the MAPPs can be accessed from <http://www.databases.niper.ac.in/pombe>.
- System Requirements for GenMAPP 2.0/2.1 and MAPPFinder 2.0:
Operating System: Windows 98 or higher, Windows NT 4.0 or higher (2000, XP, etc)
Monitor Resolution: 800 X 600 screen or greater (SVGA)
Internet Browser: Microsoft Internet Explorer 5.0 or later
Minimum hardware configuration:
Memory: 128 MB (512 MB or more recommended)
Processor: Pentium III
Disk space: 300 MB disk (more recommended if multiple databases will be used)

3. Installation Instructions

- Download and extract the zipped archive named “pombe.zip” and place the file “Sp-Std_20060502.gdb” in the folder you use to store Gene Databases for GenMAPP. If you accept the default folder during the GenMAPP installation process, this folder will be C:\GenMAPP 2 Data\Gene Databases.
- To use the Gene Database, launch GenMAPP and go to the menu item Data > Choose Gene Database. Alternatively, you can launch MAPPFinder and go to the menu item File > Choose Gene Database.

4. Gene Database Specifications

Gene ID Systems

This *S.pombe* Gene Database was built on May 5, 2006. This build date is reflected in the filename “Spo-GO_20060502-Sp.gdb”. The main data source (primary ID system) for gene IDs and annotations of this Gene Database is the Genome Database (GeneDB) from the *S.pombe* genome project at Sanger Institute, made available for download at “http://www.sanger.ac.uk/Projects/S_pombe/download.shtml”. In addition to GeneDB IDs, encoded as SpombeGeneDB, this database provides other gene ID systems cross referenced by the *S.pombe* Genome Database. These ID systems along with their assigned system codes are listed in the table below.

S.No.	ID System	System Code	Data resource
1	SpombeGeneDB (GeneDB ID)	&b	http://www.sanger.ac.uk/Projects/S_pombe/download.shtml
2	InterProID	&n	http://www.sanger.ac.uk/Projects/S_pombe/download.shtml
3	SGDID	&s	http://www.sanger.ac.uk/Projects/S_pombe/download.shtml
4	PfamID	&p	http://www.sanger.ac.uk/Projects/S_pombe/download.shtml
5	UniProtID	&u	http://www.sanger.ac.uk/Projects/S_pombe/download.shtml
6	IUBMBID	&I	http://www.sanger.ac.uk/Projects/S_pombe/download.shtml
7	Gene Ontology	T	ftp://ftp.sanger.ac.uk/pub/yeast/pombe/Gene_ontology/gene_association.GeneDB_Spombe

The gene ontology gene association file for the species *S.pombe* were collected from the site of Sanger Institute at “ftp://ftp.sanger.ac.uk/pub/yeast/pombe/Gene_ontology/gene_association.GeneDB_Spombe”. The gene ortholog data necessary for inferring pathway MAPPs from *S. cerevisiae* was obtained from the Sanger Institute and by searching the SGD site manually for some of the genes.

5. Contact Information for support, bug reports, feature requests

For issues related to the *S.pombe* Gene Database, please contact:

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For issues related to GenMAPP 2.0/2.1 or MAPPFinder 2.0, please contact:

GenMAPP support directly by e-mailing genmapp@gladstone.ucsf.edu.